

SEQUENCE LISTING

<110> Sheppard, Paul O.
 Presnell, Scott R.
 Taft, David W.

<120> NOVEL SECRETED PROTEINS

<130> 01-26

<150> 60/215,446

<151> 2000-06-30

<160> 10

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 453

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(453)

<400> 1

atg gtg gta ttt acc ttg ctg ctg gtg ctg ctg ttg ttg ctg ctg cta	48
Met Val Val Phe Thr Leu Leu Leu Val Leu Leu Leu Leu Leu Leu	
1 5 10 15	
aca gct cta tgt aag gct ctg agt caa agc ctt ccc tat acc ctc tac	96
Thr Ala Leu Cys Lys Ala Leu Ser Gln Ser Leu Pro Tyr Thr Leu Tyr	
20 25 30	
agg cca cag tca tca cta tcc ttc ctc ctt atc act gat ata aaa aag	144
Arg Pro Gln Ser Ser Leu Ser Phe Leu Leu Ile Thr Asp Ile Lys Lys	
35 40 45	
att gat ata cag tat ttt ctc cca ttg aca ggt ggc aag tgc ctg cat	192
Ile Asp Ile Gln Tyr Phe Leu Pro Leu Thr Gly Gly Lys Cys Leu His	
50 55 60	

ctt cgc ttg aca gga cag agg gct ttc tgt atc ctg gag ttc ttg cct 240
 Leu Arg Leu Thr Gly Gln Arg Ala Phe Cys Ile Leu Glu Phe Leu Pro
 65 70 75 80

tgg tgt aat gga ata att gaa tca ctc gtg ggc ttg gag aat gag cgc 288
 Trp Cys Asn Gly Ile Ile Glu Ser Leu Val Gly Leu Glu Asn Glu Arg
 85 90 95

aag gtt ttg agt gga ggt agc tct cag cag atg ggg gaa gcc aga agg 336
 Lys Val Leu Ser Gly Gly Ser Ser Gln Gln Met Gly Glu Ala Arg Arg
 100 105 110

gga atg gag tgg gaa gtt ttt ccc ctg gag ttg ggc cgc cca gag gcc 384
 Gly Met Glu Trp Glu Val Phe Pro Leu Glu Leu Gly Arg Pro Glu Ala
 115 120 125

ggg gct ctc caa cga ctg ccc cag cca aac tcc gcg ttg ttg gct tgc 432
 Gly Ala Leu Gln Arg Leu Pro Gln Pro Asn Ser Ala Leu Leu Ala Cys
 130 135 140

cgg tgt gct ggt gcc tat tag 453
 Arg Cys Ala Gly Ala Tyr *
 145 150

<210> 2

<211> 150

<212> PRT

<213> Homo sapiens

<400> 2

Met Val Val Phe Thr Leu Leu Leu Val Leu Leu Leu Leu Leu Leu 15
 1 5 10 15
 Thr Ala Leu Cys Lys Ala Leu Ser Gln Ser Leu Pro Tyr Thr Leu Tyr
 20 25 30
 Arg Pro Gln Ser Ser Leu Ser Phe Leu Leu Ile Thr Asp Ile Lys Lys
 35 40 45
 Ile Asp Ile Gln Tyr Phe Leu Pro Leu Thr Gly Gly Lys Cys Leu His
 50 55 60
 Leu Arg Leu Thr Gly Gln Arg Ala Phe Cys Ile Leu Glu Phe Leu Pro
 65 70 75 80

Trp Cys Asn Gly Ile Ile Glu Ser Leu Val Gly Leu Glu Asn Glu Arg
 85 90 95
 Lys Val Leu Ser Gly Gly Ser Ser Gln Gln Met Gly Glu Ala Arg Arg
 100 105 110
 Gly Met Glu Trp Glu Val Phe Pro Leu Glu Leu Gly Arg Pro Glu Ala
 115 120 125
 Gly Ala Leu Gln Arg Leu Pro Gln Pro Asn Ser Ala Leu Leu Ala Cys
 130 135 140
 Arg Cys Ala Gly Ala Tyr
 145 150

<210> 3
 <211> 450
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate polynucleotide

<221> misc_feature
 <222> (1)...(450)
 <223> n = A,T,C or G

<400> 3
 atggtngtnt tyacnytnyt nytngtnytn ytnytnytny tnytnytnac ngcnytnrtgy 60
 aargcnytnw sncarwsnyt nccntayacn ytntaymgnc cncarwsnws nytnwsntty 120
 ytrytnatha cngayathaa raarathgay athcartayt tyytnccnyt nacnggnggn 180
 aartggytnc ayytnmgnyt nacnggncar mgngcnttyt gyathytnga rttyytncn 240
 tggatgyaayg gnathathga rwsnytnngtn ggnytngara aygarmgnaa rgtnytnwsn 300
 ggnggnwsnw sncarcarat gggngargcn mgnmgnggna tggartggga rgtnttyccn 360
 ytngarytn gnmgnccnga rgcngngcn ytnarmgny tncncarcc naaywsngcn 420
 ytnytnngnt gymgntgygc nggngcntay 450

<210> 4
 <211> 354
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(354)

<400> 4

atg agc cca ggc tat ttg ctg ctg ctg ctg ctg ttg gag tca cct gtt 48
 Met Ser Pro Gly Tyr Leu Leu Leu Leu Leu Leu Leu Glu Ser Pro Val
 1 5 10 15

gct gga agg aac tgt gcc act gta cta cac cag aac agc tgc cat ctc 96
 Ala Gly Arg Asn Cys Ala Thr Val Leu His Gln Asn Ser Cys His Leu
 20 25 30

cat gac aac aag cac gcg ctg gtg ctg cct gcc tgg agg gga gaa gag 144
 His Asp Asn Lys His Ala Leu Val Leu Pro Ala Trp Arg Gly Glu Glu
 35 40 45

cac aga gaa ggc att agc tac tgc cct ccc aga cgc agg aca agc gac 192
 His Arg Glu Gly Ile Ser Tyr Cys Pro Pro Arg Arg Arg Thr Ser Asp
 50 55 60

aga att tcc aac agc atc ggc tac tac ggc aac acc ttt tta ctc ttg 240
 Arg Ile Ser Asn Ser Ile Gly Tyr Tyr Gly Asn Thr Phe Leu Leu Leu
 65 70 75 80

tgc acc aaa ctg gcc gac atc tcg gaa caa gga ggg gac tgg cct tcc 288
 Cys Thr Lys Leu Ala Asp Ile Ser Glu Gln Gly Gly Asp Trp Pro Ser
 85 90 95

cag atc cac aat gcc gcg gaa gca gag cca gcc gcc tct cca ctc tcc 336
 Gln Ile His Asn Ala Ala Glu Ala Glu Pro Ala Ala Ser Pro Leu Ser
 100 105 110

gcc aac cgc gac aag taa 354
 Ala Asn Arg Asp Lys *
 115

<210> 5

<211> 117

<212> PRT

<213> Homo sapiens

<400> 5

Met Ser Pro Gly Tyr Leu Leu Leu Leu Leu Leu Leu Glu Ser Pro Val
 1 5 10 15
 Ala Gly Arg Asn Cys Ala Thr Val Leu His Gln Asn Ser Cys His Leu
 20 25 30

His Asp Asn Lys His Ala Leu Val Leu Pro Ala Trp Arg Gly Glu Glu
 35 40 45
 His Arg Glu Gly Ile Ser Tyr Cys Pro Pro Arg Arg Arg Thr Ser Asp
 50 55 60
 Arg Ile Ser Asn Ser Ile Gly Tyr Tyr Gly Asn Thr Phe Leu Leu Leu
 65 70 75 80
 Cys Thr Lys Leu Ala Asp Ile Ser Glu Gln Gly Gly Asp Trp Pro Ser
 85 90 95
 Gln Ile His Asn Ala Ala Glu Ala Glu Pro Ala Ala Ser Pro Leu Ser
 100 105 110
 Ala Asn Arg Asp Lys
 115

<210> 6
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate polynucleotide

<221> misc_feature
 <222> (1)...(351)
 <223> n = A,T,C or G

<400> 6
 atgwsnccng gntayytnyt nytnytnytn ytnytngarw snccngtngc nggnmgnaay 60
 tgygcnaeng tnytncaayca raaywsntgy cayytncaayg ayaayaarca ygcnytnngtn 120
 ytnccngcnt ggmgngnga rgarcaymgn garggnathw sntaytgycc nccnmgnmgn 180
 mgnacnwsng aymgnathws naaywsnath ggntaytayg gnaayacntt yytnytnytn 240
 tgyacnaary tngcngayat hwsngarcar ggnggngayt ggccnwsnca rathcayaay 300
 gcngcngarg cngarccngc ngcnwsnccn ytnwsngcna aymngayaa r 351

<210> 7
 <211> 558
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(558)

<400> 7

atg gcc cgg gcc agg gcc ggg gcg ctg ctg gcg ctt tgg gtg ctc ggg Met Ala Arg Ala Arg Ala Gly Ala Leu Leu Ala Leu Trp Val Leu Gly 1 5 10 15	48
gcc gcc gcg cat ccg cag tgc ctg gac ttc agg ccg ccc ttc cgg ccg Ala Ala Ala His Pro Gln Cys Leu Asp Phe Arg Pro Pro Phe Arg Pro 20 25 30	96
acg cag ccg ctg cgc ctc tgc gcg cag tac tcg gac ttc ggc tgc tgc Thr Gln Pro Leu Arg Leu Cys Ala Gln Tyr Ser Asp Phe Gly Cys Cys 35 40 45	144
gat gag ggg cgc gac gcc gag ctg acc cgc cgc ttc tgg gcc ctg gcg Asp Glu Gly Arg Asp Ala Glu Leu Thr Arg Arg Phe Trp Ala Leu Ala 50 55 60	192
agc cgc gtg gac gcc gcc gag tgg gcc gcg tgc gcc ggc tac gcg agg Ser Arg Val Asp Ala Ala Glu Trp Ala Ala Cys Ala Gly Tyr Ala Arg 65 70 75 80	240
gac ctg ctg tgc cag tcc gtg gag tgg aca gac atg caa aga gat aat Asp Leu Leu Cys Gln Ser Val Glu Trp Thr Asp Met Gln Arg Asp Asn 85 90 95	288
gaa gtc cta gcc aag ctg act ggc tgg agc gcc cct ggc gac gga gca Glu Val Leu Ala Lys Leu Thr Gly Trp Ser Ala Pro Gly Asp Gly Ala 100 105 110	336
gtg act gct gta gag aac tca ccc tgt aag cta caa gat tca atg gat Val Thr Ala Val Glu Asn Ser Pro Cys Lys Leu Gln Asp Ser Met Asp 115 120 125	384
tct gga ttg ggc ttt ggt gaa cgg agg gct ctc gtt gcc ttc cag atg Ser Gly Leu Gly Phe Gly Glu Arg Arg Ala Leu Val Ala Phe Gln Met 130 135 140	432
tct gtt ctg ccc ctc act gcg tct ctg gaa cca aga tgg tgc ctg gta Ser Val Leu Pro Leu Thr Ala Ser Leu Glu Pro Arg Trp Cys Leu Val 145 150 155 160	480
caa tct ctg ctc agt aaa ttc ttg gtg aat gaa atg ttg ctg act aat Gln Ser Leu Leu Ser Lys Phe Leu Val Asn Glu Met Leu Leu Thr Asn 165 170 175	528

ctg gaa aga aca cca gtc cag gca tca tga
 Leu Glu Arg Thr Pro Val Gln Ala Ser *
 180 185

558

<210> 8
 <211> 185
 <212> PRT
 <213> Homo sapiens

<400> 8
 Met Ala Arg Ala Arg Ala Gly Ala Leu Leu Ala Leu Trp Val Leu Gly
 1 5 10 15
 Ala Ala Ala His Pro Gln Cys Leu Asp Phe Arg Pro Pro Phe Arg Pro
 20 25 30
 Thr Gln Pro Leu Arg Leu Cys Ala Gln Tyr Ser Asp Phe Gly Cys Cys
 35 40 45
 Asp Glu Gly Arg Asp Ala Glu Leu Thr Arg Arg Phe Trp Ala Leu Ala
 50 55 60
 Ser Arg Val Asp Ala Ala Glu Trp Ala Ala Cys Ala Gly Tyr Ala Arg
 65 70 75 80
 Asp Leu Leu Cys Gln Ser Val Glu Trp Thr Asp Met Gln Arg Asp Asn
 85 90 95
 Glu Val Leu Ala Lys Leu Thr Gly Trp Ser Ala Pro Gly Asp Gly Ala
 100 105 110
 Val Thr Ala Val Glu Asn Ser Pro Cys Lys Leu Gln Asp Ser Met Asp
 115 120 125
 Ser Gly Leu Gly Phe Gly Glu Arg Arg Ala Leu Val Ala Phe Gln Met
 130 135 140
 Ser Val Leu Pro Leu Thr Ala Ser Leu Glu Pro Arg Trp Cys Leu Val
 145 150 155 160
 Gln Ser Leu Leu Ser Lys Phe Leu Val Asn Glu Met Leu Leu Thr Asn
 165 170 175
 Leu Glu Arg Thr Pro Val Gln Ala Ser
 180 185

<210> 9
 <211> 555
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Degenerate polynucleotide

<221> misc_feature

<222> (1)...(555)

<223> n = A,T,C or G

<400> 9

atggcnmgng	cnmgngcngg	ngcnytnytn	gcnytnntggg	tnytnggngc	ngcngcncay	60
ccncartggy	tngaytтымg	nccnccntty	mgncnncacnc	arccnytnmg	nytnntgygc	120
cartaywsng	ayttyggntg	ytgygaygar	ggnmngngayg	cngarytnac	nmgnmgntty	180
tgggcnytn	cnwsnmngt	ngaygcngcn	gartgggcng	cntgygcngg	ntaygcnmgn	240
gayytnytn	gycarwsngt	ngartggacn	gayatgcarm	gngayaayga	rgtnytngcn	300
aarytnacng	gntggwsngc	nccnggngay	ggngcngtna	cngcngtnga	raaywsnccn	360
tgyaarytnc	argaywsnat	ggaywsnggn	ytnggnttyg	gngarmgnmg	ngcnytnngtn	420
gcnttycara	tgwsngtnyt	nccnytnacn	gcwnsnytn	arccnmngtg	gtgyytngtn	480
carwsnytny	tnwsnaartt	yytngtnaay	garatgytny	tnacnaayyt	ngarmgnacn	540
ccngtncarg	cnwsn					555

<210> 10

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide tag

<400> 10

Glu Tyr Met Pro Met Glu

1

5